

Jacobo de la Cuesta-Zuluaga

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5922394/jacobo-de-la-cuesta-zuluaga-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

18
papers

802
citations

9
h-index

22
g-index

22
ext. papers

1,154
ext. citations

6.9
avg, IF

4.42
L-index

#	Paper	IF	Citations
18	Reclassification of <i>as comb. nov.</i> based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021 , 71,	2.2	1
17	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. <i>MSystems</i> , 2021 , 6,	7.6	5
16	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , 2020 , 5,	7.6	21
15	Syntrophy via Interspecies H Transfer between and Underlies Their Global Cooccurrence in the Human Gut. <i>MBio</i> , 2020 , 11,	7.8	43
14	Struo: a pipeline for building custom databases for common metagenome profilers. <i>Bioinformatics</i> , 2020 , 36, 2314-2315	7.2	16
13	Variants in genes of innate immunity, appetite control and energy metabolism are associated with host cardiometabolic health and gut microbiota composition. <i>Gut Microbes</i> , 2020 , 11, 556-568	8.8	4
12	Gut microbiota composition explains more variance in the host cardiometabolic risk than genetic ancestry. <i>Gut Microbes</i> , 2020 , 11, 191-204	8.8	4
11	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019 , 4,	7.6	110
10	Impact of DNA extraction, sample dilution, and reagent contamination on 16S rRNA gene sequencing of human feces. <i>Applied Microbiology and Biotechnology</i> , 2018 , 102, 403-411	5.7	31
9	Gut microbiota is associated with obesity and cardiometabolic disease in a population in the midst of Westernization. <i>Scientific Reports</i> , 2018 , 8, 11356	4.9	48
8	Higher Fecal Short-Chain Fatty Acid Levels Are Associated with Gut Microbiome Dysbiosis, Obesity, Hypertension and Cardiometabolic Disease Risk Factors. <i>Nutrients</i> , 2018 , 11,	6.7	166
7	Metformin Is Associated With Higher Relative Abundance of Mucin-Degrading <i>Akkermansia muciniphila</i> and Several Short-Chain Fatty Acid-Producing Microbiota in the Gut. <i>Diabetes Care</i> , 2017 , 40, 54-62	14.6	325
6	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. <i>Frontiers in Nutrition</i> , 2016 , 3, 26	6.2	18
5	Incorporating genome-based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes		1
4	Genomic insights into adaptations of TMA-utilizing methanogens to diverse habitats including the human gut		2
3	Large scale metagenome assembly reveals novel animal-associated microbial genomes, biosynthetic gene clusters, and other genetic diversity		2
2	Gut microbiota composition explains more variance in the host cardiometabolic risk than genetic ancestry		3

1 Age and sex-dependent patterns of gut microbial diversity in human adults

1